

# SEQUENCE LISTING

<110> CO, MAN SUNG  
MAXIMILLIANO, VASQUEZ

<120> ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND FACTOR MONOCLONAL ANTIBODY

<130> 202617US0PCT

<140> 09/273,129

<141> 2001-02-20

<150> PCT/US99/16724

<151> 1999-08-19

<150> 09/136,315

<151> 1998-08-19

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 417

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(417)

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cag tgt gag gtg aaa ctt ctc gag tct gga ggt ggc ctg gtg cag act	96
Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr	
20 25 30	

gga gga tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt	144
Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser	
35 40 45	

aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa	192
Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	
50 55 60	

tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca	240
Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro	
65 70 75 80	

tct cta aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg	288
Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr	

85										90					95					
ctg	tac	ctg	caa	atg	agt	caa	gtg	aga	tct	gag	gac	aca	gcc	ctt	tac	336				
Leu	Tyr	Leu	Gln	Met	Ser	Gln	Val	Arg	Ser	Glu	Asp	Thr	Ala	Leu	Tyr					
			100					105					110							
tac	tgt	gca	aga	cct	ccc	tac	tat	ggt	agc	tac	ggg	ggg	ttt	gct	tac	384				
Tyr	Cys	Ala	Arg	Pro	Pro	Tyr	Tyr	Gly	Ser	Tyr	Gly	Gly	Phe	Ala	Tyr					
		115					120					125								
tgg	ggc	caa	ggg	act	ctg	gtc	tct	gtc	tcg	cca						417				
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			20					25					30							
Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asp	Phe	Ser					
		35					40					45								
Arg	Phe	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu					
	50					55					60									
Trp	Ile	Gly	Glu	Val	Asn	Pro	Asp	Asn	Asn	Thr	Met	Asn	Tyr	Thr	Pro					
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Ser	Leu	Lys	Asp	Lys	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr					
				85					90					95						
Leu	Tyr	Leu	Gln	Met	Ser	Gln	Val	Arg	Ser	Glu	Asp	Thr	Ala	Leu	Tyr					
			100					105						110						
Tyr	Cys	Ala	Arg	Pro	Pro	Tyr	Tyr	Gly	Ser	Tyr	Gly	Gly	Phe	Ala	Tyr					
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 1 5 10 15  
 gat gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct 96  
 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser  
 20 25 30  
 gta tct gtg gga gaa act gtc acc atc aca tgt cga gca agt gag aat 144  
 Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn  
 35 40 45  
 att tac aat aat tta gct tgg tat cag cag aga cag gga aaa tct cct 192  
 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro  
 50 55 60  
 cag ctc ctg gtc tat gct gca aca aac tta gca gat ggt gtg cca tca 240  
 Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser  
 65 70 75 80  
 agg ttc agt ggc agt gga tca ggc aca cag tat tcc ctc aag atc gac 288  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp  
 85 90 95  
 agc ctg cag tct gaa gat ttt ggg agt tat tac tgt caa cat ttg tgg 336  
 Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp  
 100 105 110  
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Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn  
 35 40 45

Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro  
 50 55 60

Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser  
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp  
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Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp  
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Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 115 120 125

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 1 5 10 15

cag tgt gag gtg caa ctt gtc gag tct gga ggt gga cta gtg cag cct 96  
 Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
 20 25 30

gga gga tca ctg aga ctc tcc tgt gca gcc tca gga ttc gat ttt agt 144  
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser  
 35 40 45

aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg ctc gag 192  
 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
 50 55 60

tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca 240

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Ser	Leu	Lys	Asp	Lys	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	
				85				90						95		
ctg	tac	ctg	caa	atg	aac	tca	ttg	aga	gct	gag	gac	acg	gcc	gtt	tac	336
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	
			100					105					110			
tac	tgt	gca	aga	cct	ccc	tac	tat	ggg	agc	tac	ggg	ggg	ttt	gct	tac	384
Tyr	Cys	Ala	Arg	Pro	Pro	Tyr	Tyr	Gly	Ser	Tyr	Gly	Gly	Phe	Ala	Tyr	
		115					120					125				
tgg	ggc	caa	ggg	act	ctg	gtc	acc	gtc	tcc	tca						417
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
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			20					25					30			
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asp	Phe	Ser	
		35					40					45				
Arg	Phe	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	
	50					55					60					
Trp	Ile	Gly	Glu	Val	Asn	Pro	Asp	Asn	Asn	Thr	Met	Asn	Tyr	Thr	Pro	
65					70					75					80	
Ser	Leu	Lys	Asp	Lys	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	
				85					90					95		
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	
			100					105					110			
Tyr	Cys	Ala	Arg	Pro	Pro	Tyr	Tyr	Gly	Ser	Tyr	Gly	Gly	Phe	Ala	Tyr	
		115					120					125				

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
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 1 5 10 15  
 gat gcc aga tgt gac atc cag atg act cag tct cca tcc tcc cta tct 96  
 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
 20 25 30  
 gca tct gtg gga gac agg gtc acc atc aca tgt cga gca agt gag aat 144  
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn  
 35 40 45  
 att tac aat aat tta gct tgg tat cag cag aaa ccg gga aaa gct cct 192  
 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 50 55 60  
 aag cta cta gtc tat gct gca aca aac tta gca gat ggt gtg cca tca 240  
 Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser  
 65 70 75 80  
 agg ttc agt ggc agt gga tca ggc aca cag tat acc ctc acg atc agc 288  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser  
 85 90 95  
 agc ctc cag cct gag gat ttt gcg act tat tac tgt caa cat ttg tgg 336  
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp  
 100 105 110  
 act tct ccg tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa 381  
 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 115 120 125

<210> 8  
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Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser  
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn  
35 40 45

Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
50 55 60

Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser  
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser  
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp  
100 105 110

Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
115 120 125